What is claimed is:

1. A crystallized P-selectin LE.

2. The crystallized P-selectin LE of Claim 1, characterized as being in plate form with space group $P2_1$, and having unit cell parameters of a=81.0Å, b=60.8Å, c=91.4Å, and beta=103.6°.

3. A crystallized complex of P-selectin LE and SLe^x.

4. The crystallized complex of Claim 3, characterized as being in plate form with space group $P2_1$, and having unit cell parameters of a=81.1Å, b=60.5Å, c=91.4Å, and beta=103.3°.

5. A crystallized complex of E-selectin LE and SLe^x.

6. The crystallized complex of Claim 5, characterized as being in rod form with space group $P2_12_12_1$, and having unit cell parameters of a=34.5Å, b=72.4Å, and c=77.6Å.

7. A crystallized complex of P-selectin LE and a PSGL-1 peptide.

8. The crystallized complex of Claim 7, characterized as being in bipyramidal form with space group I222 and having unit cell parameters of a=63.4Å, b=96.8Å, and c=187.3Å.

9. An active site of an SLe^x binding protein or peptide, wherein said active site comprises the relative structural coordinates of amino acid residues TYR48, GLU80, ASN82, GLU92, TYR94, PRO98, SER99, ASN105,

ASP106, GLU107 and bound calcium according to Figure 3, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

10. The active site of Claim 9, wherein said active site further comprises the relative structural coordinates of amino acid residues TYR44, SER46, SER47, ALA77, ASP78, ASN79, PRO81, ASN83, ARG85, GLU88, CYS90, ILE93, LYS96, SER97, ALA100, TRP104, HIS108, LYS111 and LYS113 according to Figure 3, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

11. An active site of an SLe^x binding protein or peptide, wherein said active site comprises the relative structural coordinates of amino acid residues TYR48, GLU80, ASN82, ASN83, GLU92, TYR94, ARG97, GLU98, ASN105, ASP106, GLU107 and bound calcium according to Figure 4, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

12. The active site of Claim 11, wherein said active site further comprises the relative structural coordinates of amino acid residues TYR44, SER45, PRO46, SER47, ALA77, PRO78, GLY79, PRO81, GLU88, CYS90, LYS99, ASP100, TRP104, ARG108, LYS111 and LYS113 according to Figure 4, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

13. An active site of a PSGL-1 binding protein or peptide, wherein said active site comprises the relative structural coordinates of amino acid residues ALA9, TYR45, SER46, SER47, TYR48, GLU80, ASN82, LYS84, ARG85, GLU88, GLU92, TYR94, PRO98, SER99, ASN105, ASP106, GLU107, HIS108, LEU110, LYS111, LYS112, LYS113, HIS114 and bound strontium

according to Figure 5, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

14. The active site of Claim 13, wherein said active site further comprises the relative structural coordinates of amino acid residues SER6, THR7, LYS8, TYR10, SER11, TYR44, TYR49, TRP50, ALA77, ASP78, ASN79, PRO81, ASN83, ASN86, ASN87, CYS90, ILE93, ILE95, LYS96, SER97, ALA100, TRP104 and CYS109 according to Figure 5, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

15. A method for identifying an agent that interacts with P-selectin LE, comprising the steps of:

(a) generating a three dimensional model of P-selectin LE using the relative structural coordinates according to Figures 2, 3 or 5, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å; and

(b) employing said three-dimensional model to design or select an agent that interacts with P-selectin LE.

16. The method of Claim 15, further comprising the steps of: (c) obtaining the identified agent; and (d) contacting the identified agent with P-selectin LE in order to determine the effect the agent has on P-selectin LE activity.

17. A method for identifying an activator or inhibitor of a molecule or molecular complex comprising an SLe^x binding site, comprising the steps of:

(a) generating a three dimensional model of said molecule or molecular complex comprising an SLe^x binding site using (i) the relative structural coordinates according to Figure 3 of residues TYR48, GLU80, ASN82,

GLU92, TYR94, PRO98, SER99, ASN105, ASP106, GLU107 and bound calcium, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å, or (ii) the relative structural coordinates according to Figure 4 of amino acid residues TYR48, GLU80, ASN82, GLU92, TYR94, ARG97, GLU98, ASN105, ASP106, GLU107 and bound calcium, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å; and

(b) selecting or designing a candidate activator or inhibitor by performing computer fitting analysis of the candidate activator or inhibitor with the three dimensional model generated in step (a).

18. The method of Claim 17, wherein the relative structural coordinates according to Figure 3 further comprises amino acid residues TYR44, SER46, SER47, ALA77, ASP78, ASN79, PRO81, ASN83, ARG85, GLU88, CYS90, ILE93, LYS96, SER97, ALA100, TRP104, HIS108, LYS111 and LYS113, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

19. The method of Claim 17, wherein the relative structural coordinates according to Figure 4 further comprises the amino acid residues TYR44, SER45, PRO46, SER47, ALA77, PRO78, GLY79, PRO81, GLU88, CYS90, LYS99, ASP100, TRP104, ARG108, LYS111 and LYS113, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

20. The method of Claim 17, which further comprises the steps of: (c) obtaining the candidate activator or inhibitor; and (d) contacting the candidate activator or inhibitor with the molecule or molecular complex and determining the effect the candidate activator or inhibitor has on the molecule or molecular complex.

21. The method of Claim 20, wherein the candidate activator or inhibitor is contacted with the molecule or molecule complex in the presence of SLe^x in order to determine the effect the candidate activator or inhibitor has on binding of the molecule or molecular complex to SLe^x.

22. A method for identifying an activator or inhibitor of a molecule or molecular complex comprising a PSGL-1 binding site, comprising the steps of:

(a) generating a three dimensional model of said molecule or molecular complex comprising a PSGL-1 binding site using the relative structural coordinates according to Figure 5 of amino acid residues ALA9, TYR45, SER46, SER47, TYR48, GLU80, ASN82, LYS84, ARG85, GLU88, GLU92, TYR94, PRO98, SER99, ASN105, ASP106, GLU107, HIS108, LEU110, LYS111, LYS112, LYS113, HIS114 and bound strontium, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å; and

(b) selecting or designing a candidate activator or inhibitor by performing computer fitting analysis of the candidate activator or inhibitor with the three dimensional model generated in step (a).

23. The method of Claim 22, wherein the relative structural coordinates according to Figure 5 further comprises amino acid residues SER6, THR7, LYS8, TYR10, SER11, TYR44, TYR49, TRP50, ALA77, ASP78, ASN79, PRO81, ASN83, ASN86, ASN87,CYS90, ILE93, ILE95, LYS96, SER97, ALA100, TRP104 and CYS109, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å.

24. The method of Claim 22, which further comprises the steps of: (c) obtaining the candidate activator or inhibitor; and (d) contacting the candidate activator or inhibitor with the molecule or molecular complex and

determining the effect the candidate activator or inhibitor has on the molecule or molecular complex.

25. The method of Claim 24, wherein the candidate activator or inhibitor is contacted with the molecule or molecule complex in the presence of PSGL-1 or a PSGL-1 peptide in order to determine the effect the candidate activator or inhibitor has on binding of the molecule or molecular complex to PSGL-1 or a PSGL-1 peptide.

26. A method for identifying an agent that interacts with SLe^x, comprising the steps of:

(a) generating a three dimensional model of SLe^x using the relative structural coordinates according to Figures 3 or 4, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å; and

(b) employing said three-dimensional structure to design or select an agent that interacts with SLe^x.

27. The method of Claim 26, further comprising the steps of: (c) obtaining the identified agent; and (d) contacting the identified agent with SLe^x in order to determine the effect the agent has on SLe^x activity.

28. A method for identifying an agent that interacts with PSGL-1, comprising the steps of:

(a) generating a three dimensional model of a PSGL-1 peptide using the relative structural coordinates according to Figure 5, ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å; and

(b) employing said three-dimensional structure to design or select an agent that interacts with PSGL-1.

29. The method of Claim 28, further comprising the steps of: (c) obtaining the identified agent; and (d) contacting the identified agent with PSGL-1 or a PSGL-1 peptide in order to determine the effect the agent has on PSGL-1 or the PSGL-1 peptide activity.

30. An agent identified by the method of Claim 15.

31. An inhibitor or activator identified by the method of Claim 17.

32. An inhibitor or activator identified by the method of Claim 22.

33. An agent identified by the method of Claim 26.

34. An agent identified by the method of Claim 28.

35. A method for obtaining a crystallized complex of an E-selectin type molecule and a compound that coordinates calcium, said method comprising the steps of:

(a) contacting a crystallized E-selectin type molecule with a compound that coordinates calcium in the presence of calcium ions and PEG to form a crystallized complex of the E-selectin type molecule and said compound that coordinates calcium; and

(b) contacting said crystallized complex in the presence of a reduced concentration of calcium ions, and sufficient concentrations of PEG and an ionic salt to obtain a final crystallized complex, that upon cooling, is suitable for elucidating the three dimensional structures of the E-selectin type molecule and said compound that coordinates calcium by x-ray diffraction of said final crystallized complex.